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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/766,678

DATE: 01/23/2002

TIME: 10:05:23

Input Set : N:\Crf3\RULE60\09766678.raw.txt
Output Set: N:\CRF3\01232002\I766678.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Ullrich, Axel
6 Risau, Werner
7 Millauer, Birgit
8 Gazit, Aviv
9 Levitzki, Alex

11 (ii) TITLE OF INVENTION: Flk-1 Is A Receptor For Vascular
12 Endothelial Growth Factor

14 (iii) NUMBER OF SEQUENCES: 6

16 (iv) CORRESPONDENCE ADDRESS:

17 (A) ADDRESSEE: Pennie & Edmonds
18 (B) STREET: 1155 Avenue of the Americas
19 (C) CITY: New York
20 (D) STATE: New York
21 (E) COUNTRY: U.S.A.
22 (F) ZIP: 10036-2711

24 (v) COMPUTER READABLE FORM:

25 (A) MEDIUM TYPE: Floppy disk
26 (B) COMPUTER: IBM PC compatible
27 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
28 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

30 (vi) CURRENT APPLICATION DATA:

C--> 31 (A) APPLICATION NUMBER: US/09/766,678
C--> 32 (B) FILING DATE: 25-Jan-2001
33 (C) CLASSIFICATION:

35 (vii) PRIOR APPLICATION DATA:

36 (A) APPLICATION NUMBER: 08/193,829
37 (B) FILING DATE: 09-FEB-1994

40 (viii) ATTORNEY/AGENT INFORMATION:

41 (A) NAME: Coruzzi, Laura A.
42 (B) REGISTRATION NUMBER: 30,742
43 (C) REFERENCE/DOCKET NUMBER: 7683-060

45 (ix) TELECOMMUNICATION INFORMATION:

46 (A) TELEPHONE: (212)790-9090
47 (B) TELEFAX: (212)869-9741
48 (C) TELEX: 66141 PENNIE

51 (2) INFORMATION FOR SEQ ID NO: 1:

53 (i) SEQUENCE CHARACTERISTICS:

54 (A) LENGTH: 5470 base pairs
55 (B) TYPE: nucleic acid
56 (C) STRANDEDNESS: unknown
57 (D) TOPOLOGY: unknown

ENTERED

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W--> 59	(ii) MOLECULE TYPE: DNA						
62	(ix) FEATURE:						
63	(A) NAME/KEY: CDS						
64	(B) LOCATION: 286..4386						
67	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:						
69	TATAGGGCGA	ATTGGGTACG	GGACCCCCCT	CGAGGTCGAC	GGTATCGATA	AGCTTGATAT	60
71	CGAATTCCGGG	CCCAGACTGT	GTCCTCGCAGC	CGGGATAACC	TGGCTGACCC	GATTCCCGCGG	120
73	ACACCGCTGA	CAGCCGCGGC	TGGAGCCAGG	GCGCCGGTGC	CCCGCGCTCT	CCCCGGTCTT	180
75	GCGCTGCCGG	GGCCATACCG	CCTCTGTGAC	TTCTTGCAG	GCCAGGGACG	GAGAAGGAGT	240
77	CTGTGCCTGA	GAAACTGGGC	TCTGTGCCCA	GGCGCGAGGT	GCAGG	ATG GAG AGC	294
78				Met	Glu	Ser	
79				1			
81	AAG GCG CTG CTA GCT GTC	CTG	TGG TTC	TGC GTG	GAG ACC CGA	GCC	342
82	Lys Ala Leu Leu Ala Val	Leu Ala	Trp Phe Cys	Val Glu Thr	Arg Ala		
83	5	10	15				
85	GCC TCT GTG GGT TTG ACT GGC GAT	TTT CTC	CAT CCC	CCC AAG CTC	AGC		390
86	Ala Ser Val Gly Leu Thr Gly Asp	Phe Leu His	Pro Pro Lys	Leu Ser			
87	20	25	30	35			
89	ACA CAG AAA GAC ATA CTG ACA ATT TTG GCA AAT	ACA ACC	CTT CAG ATT				438
90	Thr Gln Lys Asp Ile Leu Thr Ile Leu Ala Asn	Thr Thr Leu Gln	Ile				
91	40	45	50				
93	ACT TGC AGG GGA CAG CGG GAC CTG GAC TGG	CTT TGG	CCC AAT GCT CAG				486
94	Thr Cys Arg Gly Gln Arg Asp Leu Asp Trp	Leu Trp Pro	Asn Ala Gln				
95	55	60	65				
97	CGT GAT TCT GAG GAA AGG GTA TTG GTG ACT GAA	TGC GGC	GGT GGT GAC				534
98	Arg Asp Ser Glu Glu Arg Val Leu Val Thr Glu	Cys Gly Gly Asp					
99	70	75	80				
101	AGT ATC TTC TGC AAA ACA CTC ACC ATT CCC	AGG GTG	GTT GGA AAT GAT				582
102	Ser Ile Phe Cys Lys Thr Leu Thr Ile Pro	Arg Val Val Gly Asn Asp					
103	85	90	95				
105	ACT GGA GCC TAC AAG TGC TCG TAC CGG GAC	GTC GAC ATA	GCC TCC ACT				630
106	Thr Gly Ala Tyr Lys Cys Ser Tyr Arg Asp	Val Asp Ile Ala Ser	Thr				
107	100	105	110	115			
109	GTT TAT GTC TAT GTT CGA GAT TAC AGA TCA	CCA TTC ATC	GCC TCT GTC				678
110	Val Tyr Val Tyr Val Arg Asp Tyr Arg Ser	Pro Phe Ile Ala Ser	Val				
111	120	125	130				
113	AGT GAC CAG CAT GGC ATC GTG TAC ATC ACC	GAG AAC AAG AAC	AAA ACT				726
114	Ser Asp Gln His Gly Ile Val Tyr Ile Thr	Glu Asn Lys Asn	Lys Thr				
115	135	140	145				
117	GTC GTG ATC CCC TGC CGA GGG TCG ATT TCA	AAC CTC AAT	GTG TCT CTT				774
118	Val Val Ile Pro Cys Arg Gly Ser Ile Ser	Asn Leu Asn Val	Ser Leu				
119	150	155	160				
121	TGC GCT AGG TAT CCA GAA AAG AGA	TTT GTT CCG	GAT GGA AAC AGA ATT				822
122	Cys Ala Arg Tyr Pro Glu Lys Arg Phe Val	Pro Asp Gly	Asn Arg Ile				
123	165	170	175				
125	TCC TGG GAC AGC GAG ATA GGC TTT ACT CTC	CCC AGT	TAC ATG ATC AGC				870
126	Ser Trp Asp Ser Glu Ile Gly Phe Thr Leu	Pro Ser Tyr Met	Ile Ser				
127	180	185	190	195			
129	TAT GCC GGC ATG GTC TTC TGT GAG GCA AAG	ATC AAT GAT	GAA ACC TAT				918

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130	Tyr Ala Gly Met Val Phe Cys Glu Ala Lys Ile Asn Asp Glu Thr Tyr			
131	200	205	210	
133	CAG TCT ATC ATG TAC ATA GTT GTG GTT GTA GGA TAT AGG ATT TAT GAT	966		
134	Gln Ser Ile Met Tyr Ile Val Val Val Gly Tyr Arg Ile Tyr Asp			
135	215	220	225	
137	GTG ATT CTG AGC CCC CCG CAT GAA ATT GAG CTA TCT GCC GGA GAA AAA	1014		
138	Val Ile Leu Ser Pro Pro His Glu Ile Glu Leu Ser Ala Gly Glu Lys			
139	230	235	240	
141	CTT GTC TTA AAT TGT ACA GCG AGA ACA GAG CTC AAT GTG GGG CTT GAT	1062		
142	Leu Val Leu Asn Cys Thr Ala Arg Thr Glu Leu Asn Val Gly Leu Asp			
143	245	250	255	
145	TTC ACC TGG CAC TCT CCA CCT TCA AAG TCT CAT CAT AAG AAG ATT GTA	1110		
146	Phe Thr Trp His Ser Pro Pro Ser Lys Ser His His Lys Lys Ile Val			
147	260	265	270	275
149	AAC CGG GAT GTG AAA CCC TTT CCT GGG ACT GTG GCG AAG ATG TTT TTG	1158		
150	Asn Arg Asp Val Lys Pro Phe Pro Gly Thr Val Ala Lys Met Phe Leu			
151	280	285	290	
153	AGC ACC TTG ACA ATA GAA AGT GTG ACC AAG AGT GAC CAA GGG GAA TAC	1206		
154	Ser Thr Leu Thr Ile Glu Ser Val Thr Lys Ser Asp Gln Gly Glu Tyr			
155	295	300	305	
157	ACC TGT GTA GCG TCC AGT GGA CGG ATG ATC AAG AGA AAT AGA ACA TTT	1254		
158	Thr Cys Val Ala Ser Ser Gly Arg Met Ile Lys Arg Asn Arg Thr Phe			
159	310	315	320	
161	GTC CGA GTT CAC ACA AAG CCT TTT ATT GCT TTC GGT AGT GGG ATG AAA	1302		
162	Val Arg Val His Thr Lys Pro Phe Ile Ala Phe Gly Ser Gly Met Lys			
163	325	330	335	
165	TCT TTG GTG GAA GCC ACA GTG GGC AGT CAA GTC CGA ATC CCT GTG AAG	1350		
166	Ser Leu Val Glu Ala Thr Val Gly Ser Gln Val Arg Ile Pro Val Lys			
167	340	345	350	355
169	TAT CTC AGT TAC CCA GCT CCT GAT ATC AAA TGG TAC AGA AAT GGA AGG	1398		
170	Tyr Leu Ser Tyr Pro Ala Pro Asp Ile Lys Trp Tyr Arg Asn Gly Arg			
171	360	365	370	
173	CCC ATT GAG TCC AAC TAC ACA ATG ATT GTT GGC GAT GAA CTC ACC ATC	1446		
174	Pro Ile Glu Ser Asn Tyr Thr Met Ile Val Gly Asp Glu Leu Thr Ile			
175	375	380	385	
177	ATG GAA GTG ACT GAA AGA GAT GCA GGA AAC TAC ACG GTC ATC CTC ACC	1494		
178	Met Glu Val Thr Glu Arg Asp Ala Gly Asn Tyr Thr Val Ile Leu Thr			
179	390	395	400	
181	AAC CCC ATT TCA ATG GAG AAA CAG AGC CAC ATG GTC TCT CTG GTT GTG	1542		
182	Asn Pro Ile Ser Met Glu Lys Gln Ser His Met Val Ser Leu Val Val			
183	405	410	415	
185	AAT GTC CCA CCC CAG ATC GGT GAG AAA GCC TTG ATC TCG CCT ATG GAT	1590		
186	Asn Val Pro Pro Gln Ile Gly Glu Lys Ala Leu Ile Ser Pro Met Asp			
187	420	425	430	435
189	TCC TAC CAG TAT GGG ACC ATG CAG ACA TTG ACA TGC ACA GTC TAC GCC	1638		
190	Ser Tyr Gln Tyr Gly Thr Met Gln Thr Leu Thr Cys Thr Val Tyr Ala			
191	440	445	450	
193	AAC CCT CCC CTG CAC CAC ATC CAG TGG TAC TGG CAG CTA GAA GAA GCC	1686		
194	Asn Pro Pro Leu His His Ile Gln Trp Tyr Trp Gln Leu Glu Ala			

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195	455	460	465	
197	TGC TCC TAC AGA CCC GGC CAA ACA AGC CCG TAT GCT TGT AAA GAA TGG			1734
198	Cys Ser Tyr Arg Pro Gly Gln Thr Ser Pro Tyr Ala Cys Lys Glu Trp			
199	470	475	480	
201	AGA CAC GTG GAG GAT TTC CAG GGG GGA AAC AAG ATC GAA GTC ACC AAA			1782
202	Arg His Val Glu Asp Phe Gln Gly Gly Asn Lys Ile Glu Val Thr Lys			
203	485	490	495	
205	AAC CAA TAT GCC CTG ATT GAA GGA AAA AAC AAA ACT GTA AGT ACG CTG			1830
206	Asn Gln Tyr Ala Leu Ile Glu Gly Lys Asn Lys Thr Val Ser Thr Leu			
207	500	505	510	515
209	GTC ATC CAA GCT GCC AAC GTG TCA GCG TTG TAC AAA TGT GAA GCC ATC			1878
210	Val Ile Gln Ala Ala Asn Val Ser Ala Leu Tyr Lys Cys Glu Ala Ile			
211	520	525	530	
213	AAC AAA GCG GGA CGA GGA GAG AGG GTC ATC TCC TTC CAT GTG ATC AGG			1926
214	Asn Lys Ala Gly Arg Gly Glu Arg Val Ile Ser Phe His Val Ile Arg			
215	535	540	545	
217	GGT CCT GAA ATT ACT GTG CAA CCT GCT GCC CAG CCA ACT GAG CAG GAG			1974
218	Gly Pro Glu Ile Thr Val Gln Pro Ala Ala Gln Pro Thr Glu Gln Glu			
219	550	555	560	
221	AGT GTG TCC CTG TTG TGC ACT GCA GAC AGA AAT ACG TTT GAG AAC CTC			2022
222	Ser Val Ser Leu Leu Cys Thr Ala Asp Arg Asn Thr Phe Glu Asn Leu			
223	565	570	575	
225	ACG TGG TAC AAG CTT GGC TCA CAG GCA ACA TCG GTC CAC ATG GGC GAA			2070
226	Thr Trp Tyr Lys Leu Gly Ser Gln Ala Thr Ser Val His Met Gly Glu			
227	580	585	590	595
229	TCA CTC ACA CCA GTT TGC AAG AAC TTG GAT GCT CTT TGG AAA CTG AAT			2118
230	Ser Leu Thr Pro Val Cys Lys Asn Leu Asp Ala Leu Trp Lys Leu Asn			
231	600	605	610	
233	GGC ACC ATG TTT TCT AAC AGC ACA AAT GAC ATC TTG ATT GTG GCA TTT			2166
234	Gly Thr Met Phe Ser Asn Ser Thr Asn Asp Ile Leu Ile Val Ala Phe			
235	615	620	625	
237	CAG AAT GCC TCT CTG CAG GAC CAA GGC GAC TAT GTT TGC TCT GCT CAA			2214
238	Gln Asn Ala Ser Leu Gln Asp Gln Gly Asp Tyr Val Cys Ser Ala Gln			
239	630	635	640	
241	GAT AAG AAG ACC AAG AAA AGA CAT TGC CTG GTC AAA CAG CTC ATC ATC			2262
242	Asp Lys Lys Thr Lys Arg His Cys Leu Val Lys Gln Leu Ile Ile			
243	645	650	655	
245	CTA GAG CGC ATG GCA CCC ATG ATC ACC GGA AAT CTG GAG AAT CAG ACA			2310
246	Leu Glu Arg Met Ala Pro Met Ile Thr Gly Asn Leu Glu Asn Gln Thr			
247	660	665	670	675
249	ACA ACC ATT GGC GAG ACC ATT GAA GTG ACT TGC CCA GCA TCT GGA AAT			2358
250	Thr Thr Ile Gly Glu Thr Ile Glu Val Thr Cys Pro Ala Ser Gly Asn			
251	680	685	690	
253	CCT ACC CCA CAC ATT ACA TGG TTC AAA GAC AAC GAG ACC CTG GTA GAA			2406
254	Pro Thr Pro His Ile Thr Trp Phe Lys Asp Asn Glu Thr Leu Val Glu			
255	695	700	705	
257	GAT TCA GGC ATT GTA CTG AGA GAT GGG AAC CGG AAC CTG ACT ATC CGC			2454
258	Asp Ser Gly Ile Val Leu Arg Asp Gly Asn Arg Asn Leu Thr Ile Arg			
259	710	715	720	

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261	AGG	GTG	AGG	AAG	GAG	GAT	GGA	GGC	CTC	TAC	ACC	TGC	CAG	GCC	TGC	AAT	2502
262	Arg	Val	Arg	Lys	Glu	Asp	Gly	Gly	Leu	Tyr	Thr	Cys	Gln	Ala	Cys	Asn	
263	725			730					735								
265	GTC	CTT	GGC	TGT	GCA	AGA	GCG	GAG	ACG	CTC	TTC	ATA	ATA	GAA	GGT	GCC	2550
266	Val	Leu	Gly	Cys	Ala	Arg	Ala	Glu	Thr	Leu	Phe	Ile	Ile	Glu	Gly	Ala	
267	740			745					750			755					
269	CAG	GAA	AAG	ACC	AAC	TTG	GAA	GTC	ATT	ATC	CTC	GTC	GGC	ACT	GCA	GTG	2598
270	Gln	Glu	Lys	Thr	Asn	Leu	Glu	Val	Ile	Ile	Leu	Val	Gly	Thr	Ala	Val	
271		760			765				770								
273	ATT	GCC	ATG	TTC	TTC	TGG	CTC	CTT	GTC	ATT	GTC	CTA	CGG	ACC	GTT	2646	
274	Ile	Ala	Met	Phe	Phe	Trp	Leu	Leu	Leu	Val	Ile	Val	Leu	Arg	Thr	Val	
275		775			780				785								
277	AAG	CGG	GCC	AAT	GAA	GGG	GAA	CTG	AAG	ACA	GGC	TAC	TTG	TCT	ATT	GTC	2694
278	Lys	Arg	Ala	Asn	Glu	Gly	Glu	Leu	Lys	Thr	Gly	Tyr	Leu	Ser	Ile	Val	
279		790			795				800								
281	ATG	GAT	CCA	GAT	GAA	TTG	CCC	TTG	GAT	GAG	CGC	TGT	GAA	CGC	TTG	CCT	2742
282	Met	Asp	Pro	Asp	Glu	Leu	Pro	Leu	Asp	Glu	Arg	Cys	Glu	Arg	Leu	Pro	
283		805			810				815								
285	TAT	GAT	GCC	AGC	AAG	TGG	GAA	TTC	CCC	AGG	GAC	CGG	CTG	AAA	CTA	GGA	2790
286	Tyr	Asp	Ala	Ser	Lys	Trp	Glu	Phe	Pro	Arg	Asp	Arg	Leu	Lys	Leu	Gly	
287	820		825			830			835								
289	AAA	CCT	CTT	GGC	CGC	GGT	GCC	TTC	GGC	CAA	GTG	ATT	GAG	GCA	GAC	GCT	2838
290	Lys	Pro	Leu	Gly	Arg	Gly	Ala	Phe	Gly	Gln	Val	Ile	Glu	Ala	Asp	Ala	
291		840			845				850								
293	TTT	GGA	ATT	GAC	AAG	ACA	GCG	ACT	TGC	AAA	ACA	GTA	GCC	GTC	AAG	ATG	2886
294	Phe	Gly	Ile	Asp	Lys	Thr	Ala	Thr	Cys	Lys	Thr	Val	Ala	Val	Lys	Met	
295		855			860				865								
297	TTG	AAA	GAA	GGA	GCA	ACA	CAC	AGC	GAG	CAT	CGA	GCC	CTC	ATG	TCT	GAA	2934
298	Leu	Lys	Glu	Gly	Ala	Thr	His	Ser	Glu	His	Arg	Ala	Leu	Met	Ser	Glu	
299		870			875				880								
301	CTC	AAG	ATC	CTC	ATC	CAC	ATT	GGT	CAC	CAT	CTC	AAT	GTG	GTG	AAC	CTC	2982
302	Leu	Lys	Ile	Leu	Ile	His	Ile	Gly	His	His	Leu	Asn	Val	Val	Asn	Leu	
303		885			890				895								
305	CTA	GGC	GCC	TGC	ACC	AAG	CCG	GGA	GGG	CCT	CTC	ATG	GTG	ATT	GTG	GAA	3030
306	Leu	Gly	Ala	Cys	Thr	Lys	Pro	Gly	Gly	Pro	Leu	Met	Val	Ile	Val	Glu	
307	900		905			910			915								
309	TTC	TGC	AAG	TTT	GGA	AAC	CTA	TCA	ACT	TAC	TTA	CGG	GGC	AAG	AGA	AAT	3078
310	Phe	Cys	Lys	Phe	Gly	Asn	Leu	Ser	Thr	Tyr	Leu	Arg	Gly	Lys	Arg	Asn	
311		920			925				930								
313	GAA	TTT	GTT	CCC	TAT	AAG	AGC	AAA	GGG	GCA	CGC	TTC	CGC	CAG	GGC	AAG	3126
314	Glu	Phe	Val	Pro	Tyr	Lys	Ser	Lys	Gly	Ala	Arg	Phe	Arg	Gln	Gly	Lys	
315		935			940				945								
317	GAC	TAC	GTT	GGG	GAG	CTC	TCC	GTG	GAT	CTG	AAA	AGA	CGC	TTG	GAC	AGC	3174
318	Asp	Tyr	Val	Gly	Glu	Leu	Ser	Val	Asp	Leu	Lys	Arg	Arg	Leu	Asp	Ser	
319		950			955				960								
321	ATC	ACC	AGC	AGC	CAG	AGC	TCT	GCC	AGC	TCA	GGC	TTT	GTT	GAG	GAG	AAA	3222
322	Ile	Thr	Ser	Ser	Gln	Ser	Ser	Ala	Ser	Ser	Gly	Phe	Val	Glu	Glu	Lys	
323		965			970				975								
325	TCG	CTC	AGT	GAT	GTA	GAG	GAA	GAA	GCT	TCT	GAA	GAA	CTG	TAC	AAG		3270

VERIFICATION SUMMARY
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L:31 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:32 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:59 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=1
L:740 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=3
L:756 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=4